

Untitled

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 23:12:17 ; Search time 1331.5 Seconds
(without alignments)
144.524 Million cell updates/sec

Title: US-09-856-850A-1
Perfect score: 31
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6054689 seqs, 3103772919 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

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- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Page 1

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Result No.	Score	Query Match	Length	DB	ID	Description
1	18	58.1	774	17	US-10-369-493-24648	Sequence 24648, A
2	17	54.8	1773	19	US-10-437-963-29615	Sequence 29615, A
3	17	54.8	309996	20	US-10-719-993-6785	Sequence 6785, Ap
c 4	16	51.6	297	20	US-10-425-115-180302	Sequence 180302,
c 5	16	51.6	453	20	US-10-425-115-141023	Sequence 141023,
6	16	51.6	1362	17	US-10-369-493-35509	Sequence 35509, A
c 7	16	51.6	1893	14	US-10-183-116-98	Sequence 98, Appl
c 8	16	51.6	1893	21	US-10-957-135-98	Sequence 98, Appl
c 9	15	48.4	265	18	US-10-424-599-50484	Sequence 50484, A
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c 13	15	48.4	527	20	US-10-363-345A-24895	Sequence 24895, A
14	15	48.4	527	20	US-10-363-345A-24896	Sequence 24896, A
c 15	15	48.4	527	21	US-10-363-483A-24895	Sequence 24895, A
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c 20	15	48.4	1287	19	US-10-437-963-71203	Sequence 71203, A
21	15	48.4	1389	17	US-10-282-122A-35888	Sequence 35888, A
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c 24	15	48.4	7075	8	US-08-781-986A-263	Sequence 263, App
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c 26	15	48.4	8561	13	US-10-116-048-3	Sequence 3, Appli
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 13:51:32 ; Search time 2265 Seconds
(without alignments)
558.726 Million cell updates/sec

Title: US-09-856-850A-1
Perfect score: 31
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 45554873 seqs, 20411521753 residues

Word size : 0

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	100.0	31	36	US-09-856-850A-1	Sequence 1, Appli
2	18	58.1	774	36	US-09-856-850A-17	Sequence 17, Appl
3	18	58.1	774	53	US-10-369-493-24648	Sequence 24648, A
4	18	58.1	774	106	US-60-360-039-24648	Sequence 24648, A
5	18	58.1	2398	63	US-10-834-967-1397	Sequence 1397, Ap
6	17	54.8	199	13	US-08-791-173-1041	Sequence 1041, Ap
7	17	54.8	199	25	US-09-540-229-79879	Sequence 79879, A
8	17	54.8	199	70	US-60-011-001-1041	Sequence 1041, Ap
9	17	54.8	292	5	US-07-952-911-4208	Sequence 4208, Ap
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11	17	54.8	402	40	US-09-925-552-6928	Sequence 6928, Ap
12	17	54.8	402	46	US-10-032-354-6928	Sequence 6928, Ap
13	17	54.8	409	21	US-09-362-510-40560	Sequence 40560, A
14	17	54.8	409	21	US-09-362-510A-40560	Sequence 40560, A
15	17	54.8	409	39	US-09-904-013-40560	Sequence 40560, A
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17	17	54.8	447	26	US-09-572-409-15921	Sequence 15921, A
18	17	54.8	1773	54	US-10-437-963-29615	Sequence 29615, A
19	17	54.8	2233	54	US-10-449-902-19557	Sequence 19557, A
c 20	17	54.8	3847	28	US-09-620-392-20371	Sequence 20371, A

					Untitled		
	21	17	54.8	32768	91	US-60-229-525-180	Sequence 180, App
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Untitled

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 14:49:18 ; Search time 1633 Seconds
(without alignments)
83.940 Million cell updates/sec

Title: US-09-856-850A-1
Perfect score: 31
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13003524 seqs, 2210865434 residues

Word size : 0

Total number of hits satisfying chosen parameters: 26007048

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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12: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
14: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq3:*
15: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	17	54.8	66419	11	US-10-990-328A-97807
2	17	54.8	309996	11	US-10-990-328A-94148
c 3	16	51.6	1893	13	US-11-083-611-98
4	16	51.6	5247	12	US-11-097-143-42109
5	16	51.6	10219	12	US-11-097-143-27424
6	16	51.6	310813	11	US-10-990-328A-93854
c 7	15	48.4	81	9	US-10-708-952A-386904
8	15	48.4	201	11	US-10-990-328A-427993

Untitled									
c	9	15	48.4	383	9	US-10-703-032-40429	Sequence 40429, A		
	10	15	48.4	480	9	US-10-703-032-89969	Sequence 89969, A		
	11	15	48.4	600	9	US-10-972-079-6979	Sequence 6979, Ap		
	12	15	48.4	601	11	US-10-940-774A-37434	Sequence 37434, A		
	13	15	48.4	601	11	US-10-940-774A-37435	Sequence 37435, A		
	14	15	48.4	601	11	US-10-940-774A-37436	Sequence 37436, A		
	15	15	48.4	601	11	US-10-940-774A-37437	Sequence 37437, A		
	16	15	48.4	601	11	US-10-940-774A-122472	Sequence 122472, A		
	17	15	48.4	601	11	US-10-940-774A-195618	Sequence 195618, A		
	18	15	48.4	601	11	US-10-940-774A-195619	Sequence 195619, A		
	19	15	48.4	601	11	US-10-940-774A-195620	Sequence 195620, A		
	20	15	48.4	601	11	US-10-940-774A-195621	Sequence 195621, A		
	21	15	48.4	1859	15	US-60-655-875-4011	Sequence 4011, Ap		
c	22	15	48.4	1935	15	US-60-655-875-8933	Sequence 8933, Ap		
c	23	15	48.4	3912	8	US-10-450-763-24996	Sequence 24996, A		
	24	15	48.4	8433	12	US-11-097-143-37921	Sequence 37921, A		
	25	15	48.4	28067	11	US-10-990-328A-96410	Sequence 96410, A		
c	26	15	48.4	31390	11	US-10-940-774A-15193	Sequence 15193, A		
c	27	15	48.4	39814	11	US-10-990-328A-96736	Sequence 96736, A		
c	28	15	48.4	101813	11	US-10-990-328A-94049	Sequence 94049, A		
c	29	15	48.4	110402	11	US-10-940-774A-17295	Sequence 17295, A		
c	30	15	48.4	110403	11	US-10-940-774A-12741	Sequence 12741, A		
	31	15	48.4	116609	11	US-10-990-328A-94541	Sequence 94541, A		
	32	15	48.4	165627	12	US-11-121-086-89	Sequence 89, App1		
	33	14	45.2	24	8	US-10-605-924-458847	Sequence 458847, A		
	34	14	45.2	25	12	US-11-121-849-431365	Sequence 431365, A		
c	35	14	45.2	25	13	US-11-036-317-527419	Sequence 527419, A		
	36	14	45.2	26	9	US-10-942-698-33	Sequence 33, App1		
	37	14	45.2	214	15	US-60-655-875-112621	Sequence 112621, A		
	38	14	45.2	239	9	US-10-703-032-38442	Sequence 38442, A		
c	39	14	45.2	395	15	US-60-655-875-109870	Sequence 109870, A		
c	40	14	45.2	447	9	US-10-467-657-6109	Sequence 6109, Ap		
c	41	14	45.2	447	9	US-10-467-657-7549	Sequence 7549, Ap		
c	42	14	45.2	447	9	US-10-467-657A-6109	Sequence 6109, Ap		
c	43	14	45.2	447	9	US-10-467-657A-7549	Sequence 7549, Ap		
c	44	14	45.2	458	1	PCT-US05-00517-2820	Sequence 2820, Ap		
	45	14	45.2	488	15	US-60-655-875-92606	Sequence 92606, A		

Untitled

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 23:12:17 ; Search time 1331.5 Seconds
(without alignments)
144.524 Million cell updates/sec

Title: US-09-856-850A-2
Perfect score: 31
Sequence: 1 ttgttcactgcagctacacgtcaaacacagc 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6054689 seqs, 3103772919 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

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Result No.	Score	Query Match	Length	DB	ID	Description
c 1	18	58.1	774	17	US-10-369-493-24648	Sequence 24648, A
2	17	54.8	232	11	US-09-987-899-5292	Sequence 5292, Ap
c 3	16	51.6	218	18	US-10-424-599-1042	Sequence 1042, Ap
c 4	16	51.6	493	9	US-09-783-590-539	Sequence 539, App
5	16	51.6	629	20	US-10-425-115-81902	Sequence 81902, A
c 6	16	51.6	807	17	US-10-369-493-45751	Sequence 45751, A
7	16	51.6	1153	20	US-10-425-115-131687	Sequence 131687,
8	16	51.6	4617	15	US-10-201-481-16	Sequence 16, Appl
9	16	51.6	4687	17	US-10-108-260A-1404	Sequence 1404, Ap
10	16	51.6	8439	13	US-10-194-163-473	Sequence 473, App
11	16	51.6	215221	13	US-10-087-192-1360	Sequence 1360, Ap
c 12	16	51.6	247544	19	US-10-322-696-55	Sequence 55, Appl
c 13	16	51.6	418550	17	US-10-292-798-1463	Sequence 1463, Ap
14	16	51.6	1691139	14	US-10-067-514-1	Sequence 1, Appli
15	16	51.6	1691139	17	US-10-419-723-1	Sequence 1, Appli
c 16	15	48.4	24	10	US-09-940-185-1563	Sequence 1563, Ap
17	15	48.4	60	10	US-09-908-975-13816	Sequence 13816, A
18	15	48.4	201	20	US-10-719-993-8974	Sequence 8974, Ap
c 19	15	48.4	404	14	US-10-198-846-12204	Sequence 12204, A
c 20	15	48.4	473	9	US-09-864-761-598	Sequence 598, App
21	15	48.4	554	9	US-09-764-864-606	Sequence 606, App
c 22	15	48.4	609	13	US-10-027-632-161350	Sequence 161350,
c 23	15	48.4	609	13	US-10-027-632-161351	Sequence 161351,
c 24	15	48.4	609	17	US-10-027-632-161350	Sequence 161350,
c 25	15	48.4	609	17	US-10-027-632-161351	Sequence 161351,
26	15	48.4	618	17	US-10-264-237-1046	Sequence 1046, Ap
c 27	15	48.4	677	20	US-10-363-345A-21687	Sequence 21687, A
28	15	48.4	677	20	US-10-363-345A-21688	Sequence 21688, A
c 29	15	48.4	677	21	US-10-363-483A-21687	Sequence 21687, A
30	15	48.4	677	21	US-10-363-483A-21688	Sequence 21688, A
31	15	48.4	696	9	US-09-939-980-2	Sequence 2, Appli
32	15	48.4	699	18	US-10-424-599-27788	Sequence 27788, A
c 33	15	48.4	777	20	US-10-425-115-26738	Sequence 26738, A
c 34	15	48.4	894	14	US-10-198-846-4280	Sequence 4280, Ap
c 35	15	48.4	1026	18	US-10-425-114-7311	Sequence 7311, Ap
36	15	48.4	1177	16	US-10-231-417-127	Sequence 127, App
c 37	15	48.4	1198	20	US-10-425-115-68035	Sequence 68035, A
38	15	48.4	1297	13	US-10-027-632-124548	Sequence 124548,
39	15	48.4	1297	13	US-10-027-632-124549	Sequence 124549,
40	15	48.4	1297	13	US-10-027-632-124550	Sequence 124550,
41	15	48.4	1297	17	US-10-027-632-124548	Sequence 124548,
42	15	48.4	1297	17	US-10-027-632-124549	Sequence 124549,
43	15	48.4	1297	17	US-10-027-632-124550	Sequence 124550,
44	15	48.4	1353	13	US-10-114-893-57	Sequence 57, Appl
c 45	15	48.4	1368	21	US-10-470-048B-316	Sequence 316, App

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 13:51:32 ; Search time 2265 Seconds
(without alignments)
558.726 Million cell updates/sec

Title: US-09-856-850A-2
Perfect score: 31
Sequence: 1 ttgttcactgcagctacacgtcaaacacagc 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 45554873 seqs, 20411521753 residues

Word size : 0

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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- 6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
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108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
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113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*
117: /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
118: /cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
119: /cgn2_6/ptodata/1/pna/US6049_COMB.seq:*
120: /cgn2_6/ptodata/1/pna/US6050_COMB.seq:*
121: /cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
122: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
123: /cgn2_6/ptodata/1/pna/US6053_COMB.seq:*
124: /cgn2_6/ptodata/1/pna/US6054_COMB.seq:*
125: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
126: /cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
127: /cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
128: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	31	100.0	31	36	US-09-856-850A-2	Sequence 2, Appli
c 2	18	58.1	774	36	US-09-856-850A-17	Sequence 17, Appl
c 3	18	58.1	774	53	US-10-369-493-24648	Sequence 24648, A
c 4	18	58.1	774	106	US-60-360-039-24648	Sequence 24648, A
5	18	58.1	1274	2	PCT-US03-41761-46495	Sequence 46495, A
6	18	58.1	1274	2	PCT-US03-41766A-46495	Sequence 46495, A
7	18	58.1	1274	62	US-10-750-622-46495	Sequence 46495, A
c 8	18	58.1	2398	63	US-10-834-967-1397	Sequence 1397, Ap
9	17	54.8	232	19	US-09-262-979-5292	Sequence 5292, Ap
10	17	54.8	232	20	US-09-304-517A-120062	Sequence 120062,
11	17	54.8	232	21	US-09-371-146A-120062	Sequence 120062,
12	17	54.8	232	45	US-09-985-678-120062	Sequence 120062,
13	17	54.8	232	45	US-09-987-899-5292	Sequence 5292, Ap
14	17	54.8	233	19	US-09-263-191-7691	Sequence 7691, Ap
15	17	54.8	233	44	US-09-975-254-7691	Sequence 7691, Ap
16	17	54.8	15609	116	US-60-466-412-87324	Sequence 87324, A
17	17	54.8	15609	118	US-60-487-610-19916	Sequence 19916, A
18	17	54.8	15609	128	US-60-582-609-19916	Sequence 19916, A
c 19	16	51.6	25	42	US-09-953-570A-77964	Sequence 77964, A
c 20	16	51.6	25	65	US-10-934-048A-2609	Sequence 2609, Ap
21	16	51.6	201	67	US-10-990-328-296879	Sequence 296879,

					Untitled	
c	22	16	51.6	218	26	US-09-565-240-22485
c	23	16	51.6	218	29	US-09-654-617-71582
c	24	16	51.6	218	31	US-09-684-016-71582
c	25	16	51.6	218	54	US-10-424-599-1042
	26	16	51.6	275	26	US-09-565-240-34638
	27	16	51.6	275	82	US-60-133-691-2242
	28	16	51.6	294	58	US-10-603-113-1478
	29	16	51.6	294	78	US-60-096-409-1478
	30	16	51.6	308	21	US-09-394-745-18199
	31	16	51.6	308	26	US-09-565-306-40772
	32	16	51.6	308	29	US-09-654-617-322659
	33	16	51.6	308	31	US-09-684-016-322659
	34	16	51.6	423	19	US-09-270-849B-166816
	35	16	51.6	440	29	US-09-654-617-268000
	36	16	51.6	440	31	US-09-684-016-268000
c	37	16	51.6	493	9	US-08-346-731-539
c	38	16	51.6	493	10	US-08-420-856-539
c	39	16	51.6	493	10	US-08-420-856A-539
c	40	16	51.6	493	10	US-08-420-856-539
c	41	16	51.6	493	34	US-09-783-590-539
c	42	16	51.6	493	39	US-09-912-293-7903
	43	16	51.6	601	41	US-09-947-907-3780
	44	16	51.6	601	66	US-10-940-774-157614
	45	16	51.6	629	54	US-10-425-115-81902

Sequence 22485, A
Sequence 71582, A
Sequence 71582, A
Sequence 1042, Ap
Sequence 34638, A
Sequence 2242, Ap
Sequence 1478, Ap
Sequence 1478, Ap
Sequence 18199, A
Sequence 40772, A
Sequence 322659,
Sequence 322659,
Sequence 166816,
Sequence 268000,
Sequence 268000,
Sequence 539, App
Sequence 539, App
Sequence 539, App
Sequence 539, App
Sequence 539, App
Sequence 7903, Ap
Sequence 3780, Ap
Sequence 157614,
Sequence 81902, A

Untitled

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 14:49:18 ; Search time 1633 Seconds
(without alignments)
83.940 Million cell updates/sec

Title: US-09-856-850A-2
Perfect score: 31
Sequence: 1 ttgttcactgcagctacacgtcaaacacagc 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13003524 seqs, 2210865434 residues

Word size : 0

Total number of hits satisfying chosen parameters: 26007048

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq2:*
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq4:*
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq5:*
12: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
14: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq3:*
15: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	16	51.6	25	9	US-10-932-182A-137239	Sequence 137239,
2	16	51.6	201	11	US-10-990-328A-296879	Sequence 296879,
c 3	16	51.6	549	9	US-10-932-182A-80206	Sequence 80206, A
4	16	51.6	601	11	US-10-940-774A-157614	Sequence 157614,
5	16	51.6	5643	13	US-11-003-103A-4	Sequence 4, Appli
6	16	51.6	31243	11	US-10-990-328A-96334	Sequence 96334, A
7	16	51.6	43924	11	US-10-990-328A-95069	Sequence 95069, A
8	16	51.6	87594	11	US-10-940-774A-12135	Sequence 12135, A

Untitled

	9	16	51.6	87611	11	US-10-940-774A-16139	Sequence 16139, A
	10	16	51.6	174170	11	US-10-940-774A-14810	Sequence 14810, A
	11	16	51.6	174170	11	US-10-940-774A-14811	Sequence 14811, A
	12	16	51.6	174318	11	US-10-940-774A-11880	Sequence 11880, A
	13	16	51.6	174318	11	US-10-940-774A-14812	Sequence 14812, A
	14	16	51.6	174318	11	US-10-940-774A-14813	Sequence 14813, A
	15	16	51.6	184026	11	US-10-990-328A-95311	Sequence 95311, A
c	16	16	51.6	437867	11	US-10-990-328A-96775	Sequence 96775, A
	17	16	51.6	1691139	9	US-10-255-120-1	Sequence 1, Appli
	18	16	51.6	1691140	9	US-10-868-397-1	Sequence 1, Appli
c	19	15	48.4	25	12	US-11-121-849-615060	Sequence 615060,
c	20	15	48.4	25	12	US-11-121-849-615061	Sequence 615061,
	21	15	48.4	25	13	US-11-060-756-124927	Sequence 124927,
	22	15	48.4	25	13	US-11-060-756-180300	Sequence 180300,
	23	15	48.4	201	11	US-10-990-328A-240143	Sequence 240143,
c	24	15	48.4	346	13	US-11-025-670-287	Sequence 287, App
	25	15	48.4	453	12	US-11-059-535A-1736	Sequence 1736, Ap
	26	15	48.4	453	13	US-11-059-535-1736	Sequence 1736, Ap
c	27	15	48.4	455	15	US-60-669-241-23171	Sequence 23171, A
	28	15	48.4	469	9	US-10-703-032-46600	Sequence 46600, A
c	29	15	48.4	540	9	US-10-703-032-73730	Sequence 73730, A
	30	15	48.4	544	9	US-10-972-079-78207	Sequence 78207, A
	31	15	48.4	552	9	US-10-972-079-78206	Sequence 78206, A
	32	15	48.4	599	9	US-10-972-079-78205	Sequence 78205, A
c	33	15	48.4	601	11	US-10-940-774A-74735	Sequence 74735, A
c	34	15	48.4	601	11	US-10-940-774A-74934	Sequence 74934, A
c	35	15	48.4	601	11	US-10-940-774A-75133	Sequence 75133, A
c	36	15	48.4	601	11	US-10-940-774A-75332	Sequence 75332, A
c	37	15	48.4	601	11	US-10-940-774A-75531	Sequence 75531, A
c	38	15	48.4	601	11	US-10-940-774A-106089	Sequence 106089,
c	39	15	48.4	601	11	US-10-940-774A-106288	Sequence 106288,
c	40	15	48.4	601	11	US-10-940-774A-106487	Sequence 106487,
c	41	15	48.4	601	11	US-10-940-774A-106686	Sequence 106686,
c	42	15	48.4	601	11	US-10-940-774A-106885	Sequence 106885,
	43	15	48.4	601	11	US-10-940-774A-177771	Sequence 177771,
	44	15	48.4	1335	9	US-10-703-032-34685	Sequence 34685, A
	45	15	48.4	1400	13	US-11-060-756-1693	Sequence 1693, Ap

Untitled

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OM protein - protein search, using sw model

Run on: June 16, 2005, 12:09:19 ; Search time 43 Seconds
(without alignments)
446.158 Million cell updates/sec

Title: US-09-856-850A-18
Perfect score: 257
Sequence: 1 MLKIATFNVNSIRSRLHIVI.....KPRLAEKPSDHLPLVAVFDV 257

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	3.5	298	4	US-09-252-991A-20522	Sequence 20522, A
2	8	3.1	2383	4	US-09-492-709A-302	Sequence 302, App
3	7	2.7	78	4	US-09-513-999C-7680	Sequence 7680, Ap
4	7	2.7	128	4	US-09-621-976-4077	Sequence 4077, Ap
5	7	2.7	130	3	US-09-347-819-8	Sequence 8, Appli
6	7	2.7	169	4	US-09-874-585D-50	Sequence 50, Appl
7	7	2.7	169	4	US-09-538-092-720	Sequence 720, App
8	7	2.7	281	4	US-09-248-796A-16074	Sequence 16074, A
9	7	2.7	312	4	US-09-634-238-254	Sequence 254, App
10	7	2.7	346	2	US-08-618-408B-2	Sequence 2, Appli
11	7	2.7	389	4	US-08-724-378D-2	Sequence 2, Appli
12	7	2.7	389	4	US-08-724-378D-3	Sequence 3, Appli
13	7	2.7	393	4	US-09-248-796A-14882	Sequence 14882, A
14	7	2.7	455	4	US-09-540-236-2651	Sequence 2651, Ap
15	7	2.7	479	1	US-08-665-220-2	Sequence 2, Appli
16	7	2.7	479	3	US-09-291-692-2	Sequence 2, Appli
17	7	2.7	479	3	US-09-561-756-33	Sequence 33, Appl

				Untitled	
18	7	2.7	479	3 US-09-227-721-33	Sequence 33, Appl
19	7	2.7	479	4 US-09-954-697-33	Sequence 33, Appl
20	7	2.7	479	4 US-09-009-893A-4	Sequence 4, Appli
21	7	2.7	479	4 US-09-489-155-4	Sequence 4, Appli
22	7	2.7	479	4 US-09-952-768-2	Sequence 2, Appli
23	7	2.7	521	4 US-09-962-834A-2	Sequence 2, Appli
24	7	2.7	521	4 US-09-851-873-103	Sequence 103, App
25	7	2.7	559	4 US-09-545-814-14	Sequence 14, Appl
26	7	2.7	583	4 US-09-545-814-2	Sequence 2, Appli
27	7	2.7	583	4 US-09-545-814-5	Sequence 5, Appli
28	7	2.7	635	4 US-09-545-814-32	Sequence 32, Appl
29	7	2.7	820	4 US-09-252-991A-25153	Sequence 25153, A
30	7	2.7	1233	4 US-09-252-991A-23237	Sequence 23237, A
31	7	2.7	1896	4 US-09-949-016-9508	Sequence 9508, Ap
32	6	2.3	11	4 US-09-192-854-110	Sequence 110, App
33	6	2.3	12	3 US-08-817-869-5	Sequence 5, Appli
34	6	2.3	12	5 PCT-US95-14377-5	Sequence 5, Appli
35	6	2.3	31	1 US-08-190-802A-233	Sequence 233, App
36	6	2.3	31	3 US-09-082-279B-1215	Sequence 1215, Ap
37	6	2.3	31	3 US-08-477-346-233	Sequence 233, App
38	6	2.3	31	3 US-08-473-089-233	Sequence 233, App
39	6	2.3	31	3 US-09-315-304B-1215	Sequence 1215, Ap
40	6	2.3	31	4 US-08-487-072A-233	Sequence 233, App
41	6	2.3	31	4 US-09-834-784-1215	Sequence 1215, Ap
42	6	2.3	31	4 US-09-515-965A-1215	Sequence 1215, Ap
43	6	2.3	31	4 US-09-350-641C-1215	Sequence 1215, Ap
44	6	2.3	31	4 US-09-350-841A-1215	Sequence 1215, Ap
45	6	2.3	33	4 US-09-515-965A-1950	Sequence 1950, Ap